10/526650

BT01 Rec'd PCT/PTC 0 3 MAR 2005

SEQUENCE LISTING

<110> DNAVEC RESEARCH INC.

<120> Methods of producing a viral vector comprising a membrane protein
that binds to sialic acid as a component of the envelope
using neuraminidase derived from Gram-positive bacteria

<130> D3-A0204P

<150> JP   2002-258576

<151> 2002-09-04

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1941

<212> DNA

<213> Micromonospora viridifaciens

<220>

<221> CDS

<222> (1)..(1941)

<223>

<400> 1

atg	act	gcg	aat	ccg	tac	ctc	cgc	cgc	ctg	ccc	cgg	cgc	cga	gcc	gtc	48
Met	Thr	Ala	Asn	Pro	Tyr	Leu	Arg	Arg	Leu	Pro	Arg	Arg	Arg	Ala	Val	
1				5					10					15		

agc	ttc	ctg	ctc	gca	cca	gcg	ctg	gcg	gcc	gcc	acg	gtc	gcc	ggc	gcg	96
Ser	Phe	Leu	Leu	Ala	Pro	Ala	Leu	Ala	Ala	Ala	Thr	Val	Ala	Gly	Ala	
			20				25				30					

tcc	ccc	gca	cag	gcc	atc	gcc	ggg	gca	ccc	gtc	ccg	ccc	ggc	ggc	gag	144
Ser	Pro	Ala	Gln	Ala	Ile	Ala	Gly	Ala	Pro	Val	Pro	Pro	Gly	Gly	Glu	
		35				40				45						

ccg	ctc	tac	acg	gag	cag	gac	ctc	gcc	gtg	aac	ggc	agg	gag	ggc	ttt	192
Pro	Leu	Tyr	Thr	Glu	Gln	Asp	Leu	Ala	Val	Asn	Gly	Arg	Glu	Gly	Phe	
	50				55				60							

ccg	aac	tac	cgc	atc	cca	gcg	ctg	acc	gtc	acg	ccc	gac	ggg	gac	ctg	240
Pro	Asn	Tyr	Arg	Ile	Pro	Ala	Leu	Thr	Val	Thr	Pro	Asp	Gly	Asp	Leu	
65				70				75				80				

ctg	gcc	tcg	tac	gac	ggc	cgc	ccg	acc	ggt	atc	gac	gcg	ccc	ggc	ccc	288
Leu	Ala	Ser	Tyr	Asp	Gly	Arg	Pro	Thr	Gly	Ile	Asp	Ala	Pro	Gly	Pro	
		85				90				95						

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aac tcc atc ctc caa cgc cgc agc acc gac ggc ggc cgg acg tgg ggc        336
Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly
            100                 105                 110


gag caa cag gtc gtc agc gcc ggc cag acc acc gcg ccg atc aag ggg        384
Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly
            115                 120                 125


ttc tcc gac ccc agc tac ctt gtc gac cgg gaa acc ggg acc atc ttc        432
Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe
            130                 135                 140


aac ttc cac gtc tac tcc cag cgg cag ggc ttc gcc ggc agc cgg ccc        480
Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro
145                 150                 155                 160


ggc acc gac ccg gca gac ccc aac gtg ctc cac gcc aac gtc gcg acc        528
Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr
                165                 170                 175


tcg acc gac ggc ggt ctg acc tgg tcg cac cgg acc atc acg gcc gac        576
Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp
            180                 185                 190


atc acc ccg gat ccg ggc tgg cgc agc cgc ttc gcc gcc tcc ggc gaa        624
Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu
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195   200   205

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ggc atc cag ctc cgc tat gga ccc cac gcc ggt cga ctc atc cag cag      672
Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln
    210                      215                      220
```

```
tac acg atc atc aac gct gcc ggc gcc ttc cag gcg gtg agc gtg tac      720
Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr
225                      230                      235                      240
```

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agc gac gac cac gga agg acc tgg cgc gcc ggc gaa gcc gtc ggg gtc      768
Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val
                    245                      250                      255
```

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ggc atg gac gag aac aag acc gtg gaa ctc tcc gat ggc cgg gtc ctg      816
Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu
                    260                      265                      270
```

```
ctc aac agc cgc gac tcg gcc cgc agc gga tac cgt aag gtg gcc gtc      864
Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val
                    275                      280                      285
```

```
tcc act gac ggc ggc cac agc tac ggc ccg gtg acc atc gac cgc gac      912
Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp
                    290                      295                      300
```

ctc ccc gac ccg acg aac aac gca tcg atc atc cgg gcc ttc cct gac   960
Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp
305   310   315   320

gcc ccg gcc ggc tcc gcg cgg gcc aag gtc ctg ctc ttc tcc aac gcc   1008
Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala
           325   330   335

gcc agc cag acc tcg cgc agt cag ggc acc atc cgg atg tcc tgc gac   1056
Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp
           340   345   350

gat ggc cag acc tgg ccg gtt tcg aag gtc ttc cag ccc ggc tcg atg   1104
Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met
           355   360   365

tcg tac tcc acc ctg acc gca ctg ccc gac ggc acc tac ggg ctg ctg   1152
Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu
           370   375   380

tac gag ccg ggc acc ggc atc aga tac gcc aac ttc aac ctc gcc tgg   1200
Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp
385   390   395   400

ctg ggc ggc atc tgc gcg ccc ttc acg att ccg gat gtg gcg ctc gag   1248
Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu

405   410   415

ccg ggc cag cag gtc act gtt ccg gtg gcc gtc acg aac cag tcc ggt   1296
Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly
            420   425   430

atc gcg gta ccg aag ccg agc ctt cag ctc gac gca tcg ccg gac tgg   1344
Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp
            435   440   445

cag gtt cag ggt tcc gtc gag ccc ctc atg ccc gga cgg cag gcc aag   1392
Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys
            450   455   460

ggc cag gtg acc atc acg gtt ccc gcc ggc acc acc ccc ggt cgc tac   1440
Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr
465   470   475   480

cgg gtc ggt gcg acg ctg cgc acc tcc gcg ggt aac gcg tcg acg acc   1488
Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr
            485   490   495

ttc acg gtc acg gtt gga ctg ctc gac cag gcc cgg atg agc atc gcg   1536
Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala
            500   505   510

gac gtc gac agc gag gag acc gcc cgc gaa gac ggg cgg gcg agc aac   1584

Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn

         515   520   525

gtg atc gac ggc aac ccc tcg acg ttc tgg cac acc gaa tgg tcg cgt   1632

Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg

         530   535   540

gcc gat gct cct ggc tac ccg cac cgc atc agc ctc gac ctc ggt ggc   1680

Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly

545   550   555   560

acg cac acg atc agc ggc ctc cag tac acc cga cgg cag aac agc gcc   1728

Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala

         565   570   575

aac gag cag gtc gcg gac tac gag atc tac acc agc ctg aac ggc acg   1776

Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr

         580   585   590

acc tgg gat ggc ccg gtt gcc agc ggg cgc ttc acc acg tcc ctc gcg   1824

Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala

         595   600   605

ccg cag cgc gcg gtc ttc ccg gcg cgg gac gcc agg tac atc cgg ttg   1872

Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu

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           610                 615                620

gtg gcc ctc agc gag cag acc ggg cac aag tac gcc gcg gtc gct gag        1920
Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu
625                 630                635                640


ctg gag gtg gaa ggc cag cgc                                            1941
Leu Glu Val Glu Gly Gln Arg
                645
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<212> PRT

<213> Micromonospora viridifaciens

<400> 2


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Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val
1               5                 10                15



Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Ala Thr Val Ala Gly Ala
                20                25                30
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Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu
        35   40   45

Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe
        50   55   60

Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu
65   70   75   80

Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro
                85   90   95

Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly
                100   105   110

Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly
        115   120   125

Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe
        130   135   140

Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro
145   150   155   160

Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr
            165   170   175

Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp
            180   185   190

Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu
        195   200   205

Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln
        210   215   220

Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr
225   230   235   240

Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val
          245   250   255

Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu
          260   265   270

Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val
          275   280   285

Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp
          290   295   300

Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp
305   310   315   320

Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala
          325   330   335

Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp
          340   345   350

Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met

      355   360   365

Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu

      370   375   380

Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp

385   390   395   400

Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu

            405   410   415

Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly

      420   425   430

Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp

      435   440   445

Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys
    450   455   460

Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr
465   470   475   480

Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr
       485   490   495

Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala
       500   505   510

Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn
       515   520   525

Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg
       530   535   540

Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly
545   550   555   560

Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala
              565   570   575

Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr
              580   585   590

Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala
              595   600   605

Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu
              610   615   620

Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu
625   630   635   640

Leu Glu Val Glu Gly Gln Arg
              645